

## **Abstract**

In this study, the genetic diversity of Iranian honey bee populations (*Apis mellifera* meda Skorikov, 1829) were investigated to provide information for honey bee breeding programs in future. 180 workers of honey bees were sampled from some provinces of western and central parts of Iran. Honey bee specimens were kept at 96% Ethanol and their DNAs were extracted using CTAB protocol. The DNAs were kept at -20°C for PCR amplification later. To study genetic diversity between and within populations of Iranian honey bees, PCR were run separately with 6 species specific primers namely Ap085, At003, Ag005a, Ap226, Ap207, and Ap036. These loci were amplified and PCR products were separated by electrophoresis on an 12% denaturing polyacrylamid gel. The gels were visualized utilising a modified silver staining protocol. Using the honey bee worker's genotypes, the number of alleles per locus ( $N_a$ ), effective number of alleles ( $N_e$ ), observed and expected heterozygosity ( $H_o$ ,  $H_e$ ), polymorphism information content (PIC), shannon index, and the analysis of molecular variance (AMOVA) were calculated using GenAlex software version 6.5. Our results showed that all six single locus DNA microsatellite markers were successfully amplified in this study. The overall range of the allele numbers per locus were found between 10-14 and allele size were determined in a range of 100-280 bp. The maximum values of  $N_a$  and  $N_e$  were found by Ap036 (14) while the minimum numbers of these both values were detected by Ag005a (5). The maximum (0.911) and minimum (0.617) values of  $H_o$  were found by Ap085 and Ag005a, respectively. Ap085 and Ag005a showed the highest and lowest values of  $H_e$  (0.877, 0.784, respectively). AMOVA implied that difference between the studied honey bee populations were found between and within the studied honey bee populations were insignificant. In addition, 5 and 95% genetic diversity were found between and within the studied populations of honey bees.

**Keywords:** honey bee, co-dominant, genetic diversity, population, microsatellite, polymorphism.



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**Genetic polymorphism of Iranian populations of *Apis mellifera meda* using microsatellite markers**

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